

\* \* \* \* \* STN Columbus \* \* \* \* \*

=> file caba caplus embase japio lifesci medline scisearch uspatfull

=> e chou george chin/au

E1 2 CHOU GENICHI/AU  
E2 11 CHOU GEORGE/AU  
E3 0 --> CHOU GEORGE CHIN/AU  
E4 7 CHOU GEORGE CHIN SHENG/AU  
E5 1 CHOU GEORGE I N/AU  
E6 1 CHOU GEORGE J S/AU  
E7 2 CHOU GEORGE JYH SHANN/AU  
E8 1 CHOU GEORGE T/AU  
E9 5 CHOU GER CHIH/AU  
E10 7 CHOU GERCHIH/AU  
E11 1 CHOU GI/AU  
E12 1 CHOU GIAXUNG/AU

=> s e2-e4 and (dna or nucleic)

7 FILES SEARCHED...

L1 7 ("CHOU GEORGE"/AU OR "CHOU GEORGE CHIN"/AU OR "CHOU GEORGE CHIN SHENG"/AU) AND (DNA OR NUCLEIC)

=> dup rem l1

PROCESSING COMPLETED FOR L1

L2 4 DUP REM L1 (3 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):y

L2 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1

AN 2005:98840 CAPLUS

TI Systemic delivery of non-viral vector expressing SARS viral genomic vaccine

IN \*\*\*Chou, George Chin-sheng\*\*\*

PA Taiwan

SO U.S. Pat. Appl. Publ., 21 pp.  
CODEN: USXXCO

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2005025788	A1	20050203	US 2004-860119	20040604
PRAI	US 2003-476244P	P	20030606		

AB The present invention relates to a non-viral vector for SARS Viral Genomic Vaccine. The present invention also relates to a non-targeted lipoplex or PEGylated lipoplex formulation for accumulating SARS spike genome in the lung to that results in expression of SARS spike protein. The present invention further provides a method of eliciting immunity against SARS infection, comprising: \*\*\*DNA\*\*\* vaccination using SARS spike protein in operative assocn. with a non-viral vector and subsequent local and/or systemic immunity against SARS spike protein. In the present method, the subsequent local and/or systemic immunity is primarily by s.c. administration and then followed by intra-venously boosting two weeks later.

L2 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 2

AN 2005:16961 CAPLUS

DN 142:108387

TI Apparatus, PCR primers and hybridization probe for detecting SARS coronavirus (SARS-CV) \*\*\*DNA\*\*\*

IN \*\*\*Chou, George Chin-Sheng\*\*\*

PA Asiagen Corporation, Taiwan  
SO U.S. Pat. Appl. Publ., 13 pp.  
CODEN: USXXCO  
DT Patent  
LA English  
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2005003340	A1	20050106	US 2003-609604	20030701
PRAI	US 2003-609604		20030701		

AB The present invention relates to an assay system and methods for detecting SARS coronavirus (SARS-CV) from the samples (esp. for urine) of suspected patient in the control of SARS to provide updated information of prognosis as well as the criteria for discharging a recovered patient from a hospital. The present invention provides a method for detecting SARS coronavirus (SARS-CV) \*\*\*DNA\*\*\*, obtained by the PCR amplification, from the samples. The method includes: (a) hybridizing the SARS-CV cDNA with SARS-CV-specific probes wherein the probe linked to magnetic bead; (b) transferring hybridization tubes to magnetic wells for washing; (c) adding blocking soln. into the tubes; (d) adding avidin enzyme complex or streptavidin enzyme complex into the tubes; (e) performing washing reaction to remove interfering material by the aid of magnetic field; (f) suspending magnetic beads; and (g) detecting the luminescent or color change after adding substrate of enzyme. The present invention also relates to an app. for performing the disson. of \*\*\*nucleic\*\*\* acid double strands, hybridization, washing, the sepn. of magnetic beads and thermal control in the same app. The use of this app. largely reduces the time of hybridization (less than 20 min) and the whole process of SARS-CV detection is less than 5 h.

L2 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3  
AN 2004:934226 CAPLUS  
DN 141:395432

TI Preparation of angelicin derivatives linked to acridinium-9-carboxamide derivative or biotin as \*\*\*DNA\*\*\* labeling reagents and process of preparing \*\*\*DNA\*\*\* labeling compounds  
IN \*\*\*Chou, George Chin-Sheng\*\*\*; Wu, Yu-Cheng; Hsu, Po-Ya  
PA AsiaGen Corporation, Taiwan  
SO U.S. Pat. Appl. Publ., 9 pp.  
CODEN: USXXCO

DT Patent  
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004219538	A1	20041104	US 2003-428137	20030502
	US 2004219564	A1	20041104	US 2003-689586	20031022
	US 6858742	B2	20050222		
PRAI	US 2003-428137	A3	20030502		

OS MARPAT 141:395432

AB The present invention relates to \*\*\*DNA\*\*\* labeling reagents comprising a furocoumarin deriv. and a detectable group with or without bound via a binding enhancer, and acridinium-9-carboxamide derivs. for use as chemiluminescent labels. The \*\*\*DNA\*\*\* labeling reagents are represented by formula Fu-BE-D [wherein Fu represents a furocoumarin deriv. selected from the group consisting of angelicin derivs. and psoralen derivs.; wherein BE represents none or a binding enhancer

selected from the group consisting of C4-12 alkyl, alkenyl, polyalkylamine and polyethylene glycol; and wherein D represents a detectable group selected from the group consisting of biotin, fluorescence, acridinium ester, and acridinium 9-carboxamide]. The present invention also relates to a process of prepg. \*\*\*DNA\*\*\* labeling compd. Thus, 6-(biotinylamino)hexanoic acid N-succinimide ester was condensed with angelicin deriv. (I) (R = H) in DMSO at room temp. for 36 h to give biotin-linked angelicin deriv. I (R = Q). In another expt., acridine-9-carbonyl chloride was amidated with I (R = H) in CHCl<sub>3</sub> at room temp. for 30 min to give I (R = Q1) which was methylated by Me fluorosulfate in CHCl<sub>3</sub> for 30 h to give acridinium-9-carboxamide-linked angelicin I (R = Q2).

L2 ANSWER 4 OF 4 USPTFULL on STN  
 AN 2004:280264 USPTFULL  
 TI \*\*\*DNA\*\*\* labeling reagents, acridinium-9-carboxamide derivatives and process of preparing \*\*\*DNA\*\*\* labeling compounds  
 IN \*\*\*Chou, George Chin-Sheng\*\*\*, Hsin-Shi, TAIWAN, PROVINCE OF CHINA  
 Wu, Yu-Cheng, Hsin-Shi, TAIWAN, PROVINCE OF CHINA  
 Hsu, Po-Ya, Hsin-Shi, TAIWAN, PROVINCE OF CHINA  
 PA AsiaGEN Corporation, Tainan Hsien, TAIWAN, PROVINCE OF CHINA (non-U.S. corporation)  
 PI US 2004219564 A1 20041104  
 US 6858742 B2 20050222  
 AI US 2003-689586 A1 20031022 (10)  
 RLI Division of Ser. No. US 2003-428137, filed on 2 May 2003, PENDING  
 DT Utility  
 FS APPLICATION  
 LREP BRUCE H. TROXELL, SUITE 1404, 5205 LEESBURGH PIKE, FALLS CHURCH, VA, 22041  
 CLMN Number of Claims: 20  
 ECL Exemplary Claim: 1  
 DRWN 3 Drawing Page(s)  
 LN.CNT 481

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to \*\*\*DNA\*\*\* labeling reagents comprising a furocoumarin derivative and a detectable group with or without bound via a binding enhancer, and acridinium-9-carboxamide derivatives for use as chemiluminescent labels. The present invention also relates to a process of preparing \*\*\*DNA\*\*\* labeling compound.

=> e huang chang/au

E1 2 HUANG CHANDLER M H/AU  
 E2 1 HUANG CHANDLER MARY H/AU  
 E3 19 --> HUANG CHANG/AU  
 E4 1 HUANG CHANG AN/AU  
 E5 1 HUANG CHANG BAO/AU  
 E6 1 HUANG CHANG BO/AU  
 E7 44 HUANG CHANG CANG/AU  
 E8 5 HUANG CHANG CHENG/AU  
 E9 8 HUANG CHANG CHI/AU  
 E10 1 HUANG CHANG CHING/AU  
 E11 12 HUANG CHANG CHIUN/AU  
 E12 1 HUANG CHANG CHUN/AU

=> s e3-e12 and (dna or nucleic)

L3 2 ("HUANG CHANG"/AU OR "HUANG CHANG AN"/AU OR "HUANG CHANG BAO"/AU

OR "HUANG CHANG BO"/AU OR "HUANG CHANG CANG"/AU OR "HUANG CHANG  
CHENG"/AU OR "HUANG CHANG CHI"/AU OR "HUANG CHANG CHING"/AU OR  
"HUANG CHANG CHIUN"/AU OR "HUANG CHANG CHUN"/AU) AND (DNA OR  
NUCLEIC)

=> dup rem l3

PROCESSING COMPLETED FOR L3

L4 2 DUP REM L3 (0 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 2 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 2 USPATFULL on STN

AN 2003:10683 USPATFULL

TI Erythritol-producing moniliella strains

IN Lin, Shie-Jea, Hsinchu, TAIWAN, PROVINCE OF CHINA

Wen, Chiou-Yen, Hsinchu, TAIWAN, PROVINCE OF CHINA

\*\*\*Huang, Chang-Cheng\*\*\*, Keelung, TAIWAN, PROVINCE OF CHINA

Chu, Wen-Shen, Hsinchu, TAIWAN, PROVINCE OF CHINA

PI US 2003008378 A1 20030109

AI US 2002-200730 A1 20020722 (10)

RLI Division of Ser. No. US 2001-759778, filed on 12 Jan 2001, GRANTED, Pat.  
No. US 6455301

DT Utility

FS APPLICATION

LREP Y. ROCKY TSAO, Fish & Richardson P.C., 225 Franklin Street, Boston, MA,  
02110-2804

CLMN Number of Claims: 18

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 465

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB An isolated strain of the Moniliella species that converts glucose to  
erythritol with a conversion rate of at least about 45% is disclosed, as  
is a method of producing erythritol from such a strain.

L4 ANSWER 2 OF 2 USPATFULL on STN

AN 2002:243127 USPATFULL

TI Erythritol - producing moniliella strains

IN Lin, Shie-Jea, Hsinchu, TAIWAN, PROVINCE OF CHINA

Wen, Chiou-Yen, Hsinchu, TAIWAN, PROVINCE OF CHINA

\*\*\*Huang, Chang-Cheng\*\*\*, Keelung, TAIWAN, PROVINCE OF CHINA

Chu, Wen-Shen, Hsinchu, TAIWAN, PROVINCE OF CHINA

PI US 2002132313 A1 20020919

US 6455301 B2 20020924

AI US 2001-759778 A1 20010112 (9)

DT Utility

FS APPLICATION

LREP Y. ROCKY TSAO, FISH & RICHARDSON P.C., 225 Franklin Street, Boston, MA,  
02110-2804

CLMN Number of Claims: 18

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 465

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB An isolated strain of the Moniliella species that converts glucose to  
erythritol with a conversion rate of at least about 45% is disclosed, as  
is a method of producing erythritol from such a strain.

\* \* \* \* \* STN Columbus \* \* \* \* \*

=> file caba caplus embase japio lifesci medline scisearch uspatfull

=> s (magnetic bead?) and (probe?)

L1 7227 (MAGNETIC BEAD?) AND (PROBE?)

=> dup rem l1

L2 6857 DUP REM L1 (370 DUPLICATES REMOVED)

=> s l2 and mycobact?

L3 1232 L2 AND MYCOBACT?

=> s l3 and hybridiz?

L4 1163 L3 AND HYBRIDIZ?

=> s l4 and (avidin or streptavidin)

L5 1048 L4 AND (AVIDIN OR STREPTAVIDIN)

=> s l5 and (method or assay)

L6 1048 L5 AND (METHOD OR ASSAY)

=> s l6 and (probe?(2w)magnetic bead?)

L7 15 L6 AND (PROBE?(2W) MAGNETIC BEAD?)

=> d bib 1-

YOU HAVE REQUESTED DATA FROM 15 ANSWERS - CONTINUE? Y/(N):y

L7 ANSWER 1 OF 15 USPATFULL on STN

AN 2005:10930 USPATFULL

TI Nucleic acid detection and quantification using terminal transferase based assays

IN Hassibi, Arjang, Palo Alto, CA, UNITED STATES

Ghazvini, Siavash, Menlo Park, CA, UNITED STATES

PI US 2005009064 A1 20050113

AI US 2004-844674 A1 20040513 (10)

PRAI US 2003-470347P 20030513 (60)

DT Utility

FS APPLICATION

LREP BLAKELY SOKOLOFF TAYLOR & ZAFMAN, 12400 WILSHIRE BOULEVARD, SEVENTH FLOOR, LOS ANGELES, CA, 90025-1030

CLMN Number of Claims: 35

ECL Exemplary Claim: 1

DRWN 3 Drawing Page(s)

LN.CNT 1038

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 2 OF 15 USPATFULL on STN

AN 2004:254319 USPATFULL

TI Methods and apparatus for pathogen detection, identification and/or quantification

IN Hassibi, Arjang, Palo Alto, CA, UNITED STATES

Hassibi, Babak, San Marino, CA, UNITED STATES

Ghazvini, Siavash, Menlo Park, CA, UNITED STATES

PI US 2004197845 A1 20041007

AI US 2003-627332 A1 20030724 (10)

PRAI US 2002-407412P 20020830 (60)

US 2002-422439P 20021029 (60)

US 2002-435924P 20021220 (60)

US 2002-435934P 20021220 (60)

US 2003-440670P 20030115 (60)

US 2003-451107P 20030227 (60)

US 2003-470347P 20030513 (60)  
DT Utility  
FS APPLICATION  
LREP Richard A. Nakashima, BLAKELY, SOKOLOFF, TAYLOR & ZAFMAN LLP, Seventh  
Floor, 12400 Wilshire Boulevard, Los Angeles, CA, 90025  
CLMN Number of Claims: 48  
ECL Exemplary Claim: 1  
DRWN 34 Drawing Page(s)  
LN.CNT 3755  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 3 OF 15 USPATFULL on STN  
AN 2004:254267 USPATFULL  
TI Methods and apparatus for biomolecule detection, identification,  
quantification and/or sequencing  
IN Hassibi, Arjang, Palo Alto, CA, UNITED STATES  
Hassibi, Babek, San Marino, CA, UNITED STATES  
Ghazvini, Siavash, Menlo Park, CA, UNITED STATES  
PI US 2004197793 A1 20041007  
AI US 2003-627557 A1 20030724 (10)  
PRAI US 2002-407412P 20020830 (60)  
US 2002-422439P 20021029 (60)  
US 2002-435924P 20021220 (60)  
US 2002-435934P 20021220 (60)  
US 2003-440670P 20030115 (60)  
US 2003-451107P 20030227 (60)  
US 2003-470347P 20030513 (60)

DT Utility  
FS APPLICATION  
LREP Blakely, Sokoloff, Taylor & Zafman, Seventh Floor, 12400 Wilshire  
Boulevard, Los Angeles, CA, 90025-1030  
CLMN Number of Claims: 63  
ECL Exemplary Claim: 1  
DRWN 30 Drawing Page(s)  
LN.CNT 3586  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 4 OF 15 USPATFULL on STN  
AN 2004:178318 USPATFULL  
TI Nucleic acid amplification methods  
IN Zhang, David Y., Jamaica, NY, UNITED STATES  
Zhang, Wandi, New York, NY, UNITED STATES  
Yi, Jizu, Bayside, NY, UNITED STATES  
PI US 2004137484 A1 20040715  
AI US 2003-719480 A1 20031121 (10)  
RLI Continuation-in-part of Ser. No. US 2001-978261, filed on 15 Oct 2001,  
PENDING Continuation-in-part of Ser. No. WO 2002-US32745, filed on 15  
Oct 2002, PENDING  
DT Utility  
FS APPLICATION  
LREP Steven B. Pokotilow, Stroock & Stroock & Lavan LLP, 180 Maiden Lane, New  
York, NY, 10038  
CLMN Number of Claims: 55  
ECL Exemplary Claim: 1  
DRWN 28 Drawing Page(s)  
LN.CNT 4225  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 5 OF 15 USPATFULL on STN  
AN 2004:46156 USPATFULL  
TI Nucleic acid amplification \*\*\*method\*\*\* \*\*\*hybridization\*\*\*  
signal amplification \*\*\*method\*\*\* (HSAM)  
IN Zhang, David Y., Jamaica, NY, United States  
Brandwein, Margaret, Jamaica, NY, United States  
PA Mount Sinai School of Medicine, New York, NY, United States (U.S.  
corporation)  
PI US 38442 E1 20040224  
US 5876924 19990302 (Original)  
AI US 2001-798641 20010302 (9)  
US 1996-690495 19960731 (Original)  
RLI Continuation-in-part of Ser. No. WO 1995-US7671, filed on 14 Jun 1995  
Continuation-in-part of Ser. No. US 1996-596331, filed on 20 May 1996  
Continuation-in-part of Ser. No. US 1994-263937, filed on 22 Jun 1994,  
now abandoned  
DT Reissue  
FS GRANTED  
EXNAM Primary Examiner: Siew, Jeffrey; Assistant Examiner: Tung, Joyce  
LREP Stroock & Stroock & Lavan LLP  
CLMN Number of Claims: 17  
ECL Exemplary Claim: 1,16,17  
DRWN 21 Drawing Figure(s); 13 Drawing Page(s)  
LN.CNT 3157  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 6 OF 15 USPATFULL on STN  
AN 2003:271001 USPATFULL  
TI Nucleic acid amplification \*\*\*method\*\*\* : ramification-extension  
amplification \*\*\*method\*\*\* (RAM)  
IN Zhang, David Y., Jamaica, NY, UNITED STATES  
Brandwein, Margaret, Jamaica Estates, NY, UNITED STATES  
Hsuih, Terence C.H., Long Island City, NY, UNITED STATES  
PI US 2003190604 A1 20031009  
US 6855523 B2 20050215  
AI US 2002-309438 A1 20021204 (10)  
RLI Continuation of Ser. No. US 1999-299217, filed on 23 Apr 1999, GRANTED,  
Pat. No. US 6569647 Continuation of Ser. No. US 1996-690494, filed on 31  
Jul 1996, GRANTED, Pat. No. US 5942391 Continuation-in-part of Ser. No.  
WO 1995-US7671, filed on 14 Jun 1995, PENDING Continuation-in-part of  
Ser. No. US 1994-263937, filed on 22 Jun 1994, ABANDONED  
DT Utility  
FS APPLICATION  
LREP Steven B. Pokotilow, Stroock & Stroock & Lavan LLP, 180 Maiden Lane, New  
York, NY, 10038  
CLMN Number of Claims: 46  
ECL Exemplary Claim: 1  
DRWN 13 Drawing Page(s)  
LN.CNT 3034  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 7 OF 15 USPATFULL on STN  
AN 2003:250920 USPATFULL  
TI Nucleic acid amplification methods  
IN Zhang, David Y., Jamaica, NY, UNITED STATES  
PI US 2003175706 A1 20030918

AI US 2001-978261 A1 20011015 (9)  
DT Utility  
FS APPLICATION  
LREP Steven B. Pokotilow, Esq., Stroock & Stroock & Lavan LLP, 180 Maiden  
Lane, New York, NY, 10038  
CLMN Number of Claims: 39  
ECL Exemplary Claim: 1  
DRWN 24 Drawing Page(s)  
LN.CNT 3394  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 8 OF 15 USPATFULL on STN  
AN 2003:142941 USPATFULL  
TI Nucleic acid amplification \*\*\*method\*\*\* : ramification-extension  
amplification \*\*\*method\*\*\* (RAM)  
IN Zhang, David Y., Jamaica, NY, United States  
Brandwein, Margaret, Jamaica Estates, NY, United States  
Hsuih, Terence C. H., Long Island City, NY, United States  
PA Mount Sinai School of Medicine of New York University, New York, NY,  
United States (U.S. corporation)  
PI US 6569647 B1 20030527  
AI US 1999-299217 19990423 (9)  
RLI Continuation of Ser. No. US 1996-690494, filed on 31 Jul 1996, now  
patented, Pat. No. US 5942391, issued on 24 Aug 1999  
Continuation-in-part of Ser. No. US 596331, now abandoned  
Continuation-in-part of Ser. No. US 1994-263937, filed on 22 Jun 1994,  
now abandoned  
DT Utility  
FS GRANTED  
EXNAM Primary Examiner: Whisenant, Ethan C.; Assistant Examiner: Lu, Frank  
LREP Stroock & Stroock & Lavan LLP  
CLMN Number of Claims: 33  
ECL Exemplary Claim: 1  
DRWN 21 Drawing Figure(s); 13 Drawing Page(s)  
LN.CNT 3152  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 9 OF 15 USPATFULL on STN  
AN 2002:322434 USPATFULL  
TI Nucleic acid amplification methods  
IN Zhang, David Y., Jamaica, NY, UNITED STATES  
PI US 2002182598 A1 20021205  
US 6593086 B2 20030715  
AI US 2000-728265 A1 20001201 (9)  
RLI Continuation-in-part of Ser. No. US 1999-299217, filed on 23 Apr 1999,  
PENDING Continuation of Ser. No. US 1996-690494, filed on 31 Jul 1996,  
PATENTED  
DT Utility  
FS APPLICATION  
LREP BAKER BOTIS L.L.P., 44TH FLOOR, 30 ROCKEFELLER PLAZA, NEW YORK, NY,  
10112-4498  
CLMN Number of Claims: 30  
ECL Exemplary Claim: 1  
DRWN 19 Drawing Page(s)  
LN.CNT 3841  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.



L7 ANSWER 10 OF 15 USPATFULL on STN  
AN 2002:235380 USPATFULL  
TI Two-step \*\*\*hybridization\*\*\* and capture of a polynucleotide  
IN Weisburg, William G., San Diego, CA, UNITED STATES  
Shaw, Jay H., San Diego, CA, UNITED STATES  
Becker, Michael M., San Diego, CA, UNITED STATES  
Majlessi, Mehrdad R., Escondido, CA, UNITED STATES  
Brentano, Steven T., Santee, CA, UNITED STATES  
Nunomura, Kiyotada, Tokyo, JAPAN  
PI US 2002127569 A1 20020912  
US 6534273 B2 20030318  
AI US 2001-956412 A1 20010918 (9)  
RLI Continuation-in-part of Ser. No. US 2001-910635, filed on 20 Jul 2001,  
PENDING Division of Ser. No. US 2000-574561, filed on 19 May 2000,  
GRANTED, Pat. No. US 6280952 Division of Ser. No. US 1998-70998, filed  
on 1 May 1998, GRANTED, Pat. No. US 6110678  
PRAI US 1997-45430P 19970502 (60)  
DT Utility  
FS APPLICATION  
LREP GEN PROBE INCORPORATED, 10210 GENETIC CENTER DRIVE, SAN DIEGO, CA, 92121  
CLMN Number of Claims: 20  
ECL Exemplary Claim: 1  
DRWN 7 Drawing Page(s)  
LN.CNT 2334  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 11 OF 15 USPATFULL on STN  
AN 2002:48268 USPATFULL  
TI Two-step \*\*\*hybridization\*\*\* and capture of a polynucleotide  
IN Weisburg, William G., San Diego, CA, UNITED STATES  
Shaw, Jay H., San Diego, CA, UNITED STATES  
Becker, Michael M., San Diego, CA, UNITED STATES  
Majlessi, Mehrdad, San Diego, CA, UNITED STATES  
PI US 2002028459 A1 20020307  
AI US 2001-910635 A1 20010720 (9)  
RLI Division of Ser. No. US 2000-574561, filed on 19 May 2000, GRANTED, Pat.  
No. US 6280952 Division of Ser. No. US 1998-70998, filed on 1 May 1998,  
GRANTED, Pat. No. US 6110678  
PRAI US 1997-45430P 19970502 (60)  
DT Utility  
FS APPLICATION  
LREP Christine A. Gritzmacher, GEN-PROBE INCORPORATED, Patent Department,  
10210 Genetic Center Drive, San Diego, CA, 92121  
CLMN Number of Claims: 26  
ECL Exemplary Claim: 1  
DRWN 4 Drawing Page(s)  
LN.CNT 1772  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 12 OF 15 USPATFULL on STN  
AN 2001:142094 USPATFULL  
TI Two-step \*\*\*hybridization\*\*\* and capture of a polynucleotide  
IN Weisburg, William G., San Diego, CA, United States  
Shaw, Jay H., San Diego, CA, United States  
Becker, Michael M., San Diego, CA, United States  
Majlessi, Mehrdad, San Diego, CA, United States  
PA Gen-Probe Incorporated, San Diego, CA, United States (U.S. corporation)

PI US 6280952 B1 20010828  
AI US 2000-574561 20000519 (9)  
RLI Division of Ser. No. US 1998-70998, filed on 1 May 1998, now patented,  
Pat. No. US 6110678  
DT Utility  
FS GRANTED  
EXNAM Primary Examiner: Whisenaut, Ethan  
LREP Gritzmacher, Christine, Fisher, Carlos  
CLMN Number of Claims: 20  
ECL Exemplary Claim: 1  
DRWN 7 Drawing Figure(s); 4 Drawing Page(s)  
LN.CNT 1901  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 13 OF 15 USPATFULL on STN  
AN 2000:113706 USPATFULL  
TI Two-step \*\*\*hybridization\*\*\* and capture of a polynucleotide  
IN Weisburg, William G., San Diego, CA, United States  
Shaw, Jay H., San Diego, CA, United States  
Becker, Michael M., San Diego, CA, United States  
Majlessi, Mehrdad, San Diego, CA, United States  
PA Gen-Probe Incorporated, San Diego, CA, United States (U.S. corporation)  
PI US 6110678 20000829  
AI US 1998-70998 19980501 (9)  
PRAI US 1997-45430P 19970502 (60)  
DT Utility  
FS Granted  
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Whisenant, Ethan  
LREP Gritzmacher, Christine A., Fisher, Carlos A.  
CLMN Number of Claims: 13  
ECL Exemplary Claim: 1  
DRWN 7 Drawing Figure(s); 4 Drawing Page(s)  
LN.CNT 1839  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 14 OF 15 USPATFULL on STN  
AN 1999:99539 USPATFULL  
TI Nucleic acid amplification \*\*\*method\*\*\* : ramification-extension  
amplification \*\*\*method\*\*\* (RAM)  
IN Zhang, David Y., Jamaica, NY, United States  
Brandwein, Margaret, Jamaica Estates, NY, United States  
Hsuih, Terence C. H., New York, NY, United States  
PA Mount Sinai School of Medicine, New York, NY, United States (U.S.  
corporation)  
PI US 5942391 19990824  
AI US 1996-690494 19960731 (8)  
RLI Continuation-in-part of Ser. No. WO 1995-US7671, filed on 14 Jun 1995  
which is a continuation-in-part of Ser. No. US 1994-263937, filed on 22  
Jun 1994, now abandoned  
DT Utility  
FS Granted  
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Whisenant, Ethan  
LREP Baker & Botts, LLP  
CLMN Number of Claims: 22  
ECL Exemplary Claim: 1  
DRWN 20 Drawing Figure(s); 13 Drawing Page(s)  
LN.CNT 3188

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 15 OF 15 USPATFULL on STN  
AN 1999:27388 USPATFULL  
TI Nucleic acid amplification \*\*\*method\*\*\* \*\*\*hybridization\*\*\*  
signal amplification \*\*\*method\*\*\* (HSAM)  
IN Zhang, David Y., Jamaica, NY, United States  
Brandwein, Margaret, Jamaica Estates, NY, United States  
PA Mount Sinai School of Medicine, New York, NY, United States (U.S.  
corporation)  
PI US 5876924 19990302  
AI US 1996-690495 19960731 (8)  
RLI Continuation-in-part of Ser. No. US 1996-596331, filed on 20 May 1996  
which is a continuation-in-part of Ser. No. US 1994-263937, filed on 22  
Jun 1994, now abandoned  
DT Utility  
FS Granted  
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Tung, Joyce  
LREP Baker & Botts, LLP  
CLMN Number of Claims: 15  
ECL Exemplary Claim: 1  
DRWN 21 Drawing Figure(s); 13 Drawing Page(s)  
LN.CNT 2981  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> file uspatfull  
=> s (magnetic bead?)/clm  
141775 MAGNETIC/CLM  
31497 BEAD?/CLM  
L8 459 (MAGNETIC BEAD?)/CLM  
((MAGNETIC(W) BEAD?)/CLM)  
=> s 18 and mycobact?/clm  
1645 MYCOBACT?/CLM  
L9 5 L8 AND MYCOBACT?/CLM  
=> d bib ab 1-  
YOU HAVE REQUESTED DATA FROM 5 ANSWERS - CONTINUE? Y/(N):y

L9 ANSWER 1 OF 5 USPATFULL on STN  
AN 2004:239649 USPATFULL  
TI Method of detecting pathogenic microorganism  
IN Shimada, Masamitsu, Otsu-shi, JAPAN  
Hino, Fumitsugu, Kusatsu-shi, JAPAN  
Kato, Ikunoshin, Uji-shi, JAPAN  
PI US 2004185455 A1 20040923  
AI US 2003-451882 A1 20030626 (10)  
WO 2001-JP11422 20011226  
PRAI JP 2000-396222 20001226  
JP 2000-396321 20001226  
JP 2001-199552 20010629  
JP 2001-278920 20010913  
DT Utility  
FS APPLICATION  
LREP BROWDY AND NEIMARK, P.L.L.C., 624 NINTH STREET, NW, SUITE 300,  
WASHINGTON, DC, 20001-5303  
CLMN Number of Claims: 77  
ECL Exemplary Claim: 1

DRWN 1 Drawing Page(s)

LN.CNT 3180

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Oligonucleotide probes and primers useful in detecting pathogenic microorganisms; a method of detecting a pathogenic microorganism by using the same; and kits for this method.

L9 ANSWER 2 OF 5 USPATFULL on STN

AN 2004:209355 USPATFULL

TI Sample processing

IN Chen, Shuqi, Brookline, MA, UNITED STATES  
Lemieux, Bertrand, Brighton, MA, UNITED STATES  
Wang, Zihua, Newton, MA, UNITED STATES  
Kopczynski, Kevin R., Cambridge, MA, UNITED STATES  
Chen, Lingjum, Brookline, MA, UNITED STATES

PI US 2004161788 A1 20040819

AI US 2004-773775 A1 20040205 (10)

PRAI US 2003-445304P 20030205 (60)

DT Utility

FS APPLICATION

LREP FOLEY HOAG, LLP, PATENT GROUP, WORLD TRADE CENTER WEST, 155 SEAPORT BLVD, BOSTON, MA, 02110

CLMN Number of Claims: 75

ECL Exemplary Claim: 1

DRWN 7 Drawing Page(s)

LN.CNT 2030

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A sample processing tubule may include a first segment, a second segment, and a third segment. Each segment may be defined by the tubule, may be fluidly isolated, at least in part by a breakable seal, may be so expandable as to receive a volume of fluid expelled from another segment, and may be so compressible as to contain substantially no fluid when so compressed. Each segment may contain at least one reagent.

L9 ANSWER 3 OF 5 USPATFULL on STN

AN 2001:67386 USPATFULL

TI Chip-based species identification and phenotypic characterization of microorganisms

IN Gingeras, Thomas R., Encinitas, CA, United States  
Mack, David, Menlo Park, CA, United States  
Chee, Mark S., Palo Alto, CA, United States  
Berno, Anthony J., San Jose, CA, United States  
Stryer, Lubert, Stanford, CA, United States  
Ghandour, Ghassan, Atherton, CA, United States  
Wang, Ching, San Jose, CA, United States

PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)

PI US 6228575 B1 20010508

AI US 1997-797812 19970207 (8)

RLI Continuation-in-part of Ser. No. US 1996-629031, filed on 8 Apr 1996, now abandoned

DT Utility

FS Granted

EXNAM Primary Examiner: Horlick, Kenneth R.

LREP Townsend and Townsend and Crew LLP

CLMN Number of Claims: 97

ECL Exemplary Claim: 1

DRWN 44 Drawing Figure(s); 34 Drawing Page(s)

LN.CNT 3109

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention provides oligonucleotide based arrays and methods for speciating and phenotyping organisms, for example, using oligonucleotide sequences based on the Mycobacterium tuberculosis rpoB gene. The groups or species to which an organism belongs may be determined by comparing hybridization patterns of target nucleic acid from the organism to hybridization patterns in a database.

L9 ANSWER 4 OF 5 USPATFULL on STN

AN 2000:113712 USPATFULL

TI Mismatch detection techniques

IN Kemper, Borries, Koln, Germany, Federal Republic of  
Birkenkamp-Demtroder, Karin, Solingen, Germany, Federal Republic of  
Golz, Stefan, Essen, Germany, Federal Republic of

PA Variagenics, Inc., Cambridge, MA, United States (U.S. corporation)

PI US 6110684 20000829

AI US 1999-243558 19990202 (9)

PRAI US 1998-73716P 19980204 (60)

DT Utility

FS Granted

EXNAM Primary Examiner: Myers, Carla J.; Assistant Examiner: Johannsen, Diana

LREP Clark & Elbing LLP

CLMN Number of Claims: 50

ECL Exemplary Claim: 1

DRWN 8 Drawing Figure(s); 3 Drawing Page(s)

LN.CNT 1031

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Disclosed herein is a method for detecting a mismatch in a duplex nucleic acid, involving: a) contacting the duplex nucleic acid with a reactive agent under conditions which permit the agent to bind but not cleave a mismatch in said duplex nucleic acid; b) detecting binding of the agent to the duplex nucleic acid as an indication of the presence of a mismatch in the duplex nucleic acid; c) contacting the duplex nucleic acid with the reactive agent under conditions which permit the agent to cleave a mismatch in the duplex nucleic acid; and d) detecting a cleavage product as an indication of the presence of a mismatch in the duplex nucleic acid.

L9 ANSWER 5 OF 5 USPATFULL on STN

AN 1998:111760 USPATFULL

TI Mycobacterial nucleic acid hybridization probes and methods of use

IN Guesdon, Jean-Luc, Paris, France  
Thierry, Dominique, Boulogne, France  
Ullman, Agnes, Paris, France  
Gicquel, Brigitte, Paris, France  
Brisson-Noel, Anne, Paris, France

PA Institut Pasteur, Paris, France (non-U.S. corporation)

PI US 5807672 19980915

AI US 1995-487651 19950607 (8)

RLI Continuation of Ser. No. US 1992-829016, filed on 14 Apr 1992, now patented, Pat. No. US 5597911

PRAI FR 1989-11665 19890906

FR 1990-2676 19900302

DT Utility

FS Granted

EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Tung, Joyce

LREP Oblon, Spivak, McClelland, Maier & Neustadt, P.C.  
CLMN Number of Claims: 21  
ECL Exemplary Claim: 1  
DRWN 9 Drawing Figure(s); 10 Drawing Page(s)  
LN.CNT 1173

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Fragments of nucleic acids derived from an appropriate mycobacteria genome, particularly *Mycobacterium tuberculosis*, their applications in the diagnosis of mycobacteria infections, as well as plasmides containing said fragments. The nucleotidic sequence is comprised of a nucleotidic sequence repeated in the genome of a mycobacterium and specific of the bacillus of tuberculosis and is characterized by a strong hybridation with *M. tuberculosis*.

=> s l9 and hybridiz?/clm

19652 HYBRIDIZ?/CLM

L10 3 L9 AND HYBRIDIZ?/CLM

=> d bib ab kwic

L10 ANSWER 1 OF 3 USPATFULL on STN

AN 2004:239649 USPATFULL

TI Method of detecting pathogenic microorganism

IN Shimada, Masamitsu, Otsu-shi, JAPAN

Hino, Fumitsugu, Kusatsu-shi, JAPAN

Kato, Ikunoshin, Uji-shi, JAPAN

PI US 2004185455 A1 20040923

AI US 2003-451882 A1 20030626 (10)

WO 2001-JP11422 20011226

PRAI JP 2000-396222 20001226

JP 2000-396321 20001226

JP 2001-199552 20010629

JP 2001-278920 20010913

DT Utility

FS APPLICATION

LREP BROWDY AND NEIMARK, P.L.L.C., 624 NINTH STREET, NW, SUITE 300,  
WASHINGTON, DC, 20001-5303

CLMN Number of Claims: 77

ECL Exemplary Claim: 1

DRWN 1 Drawing Page(s)

LN.CNT 3180

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Oligonucleotide probes and primers useful in detecting pathogenic microorganisms; a method of detecting a pathogenic microorganism by using the same; and kits for this method.

CLM What is claimed is:

1. probe containing the nucleotide sequence of SEQ ID NO:39 or a part thereof, which can be used to detect a \*\*\**Mycobacterium*\*\*\* tuberculosis complex \*\*\**Mycobacterium*\*\*\* tuberculosis, \*\*\**Mycobacterium*\*\*\* bovis BCG, \*\*\**Mycobacterium*\*\*\* africanum, \*\*\**Mycobacterium*\*\*\* microti and/or \*\*\**Mycobacterium*\*\*\* canetti.

2. A probe consisting of the nucleotide sequence of SEQ ID NO:11, which can be used to detect a \*\*\**Mycobacterium*\*\*\* tuberculosis complex \*\*\**Mycobacterium*\*\*\* tuberculosis, \*\*\**Mycobacterium*\*\*\* bovis BCG, \*\*\**Mycobacterium*\*\*\* africanum, \*\*\**Mycobacterium*\*\*\* microti and/or \*\*\**Mycobacterium*\*\*\* canetti.

8. A probe that can \*\*\*hybridize\*\*\* to a target nucleic acid from a pathogenic microorganism at alkaline pH.

9. The probe according to claim 8, which can \*\*\*hybridize\*\*\* to a target nucleic acid from a pathogenic microorganism at alkaline pH of 8 to 14.

10. The probe according to claim 8 or 9, wherein the pathogenic microorganism is a \*\*\*Mycobacterium\*\*\* tuberculosis complex, a gonococcus, a chlamydia or HCV.

. . . the target nucleic acid from a pathogenic microorganism is selected from a nucleotide sequence of IS 6110 gene from a \*\*\*Mycobacterium\*\*\* tuberculosis complex, a nucleotide sequence of cppB gene from a gonococcus, a nucleotide sequence of pLGV440 from a chlamydia or. . .  
. . . or a part thereof, wherein the nucleotide sequence of SEQ ID NO:39 is present in IS 6110 gene from a \*\*\*Mycobacterium\*\*\* tuberculosis complex.

. . . 21, 34 or 35, and which is fluorescence-labeled such that the fluorescence intensity is not repressed if the probe is \*\*\*hybridized\*\*\* to the target nucleic acid, and the fluorescence intensity is repressed if the probe is not \*\*\*hybridized\*\*\* to the target nucleic acid.

27. A method for detecting a pathogenic microorganism, the method comprising conducting \*\*\*hybridization\*\*\* of the probe defined by any one of claims 1 to 26 to a target nucleic acid from a pathogenic.

28. The method according to claim 27, wherein the \*\*\*hybridization\*\*\* to a target nucleic acid from a pathogenic microorganism is conducted at alkaline pH.

29. The method according to 27 or 28, wherein the pathogenic microorganism is a \*\*\*Mycobacterium\*\*\* tuberculosis complex, a gonococcus, a chlamydia or HCV.

. . . method according to claim 29, wherein the target nucleic acid from a pathogenic microorganism is IS 6110 gene from a \*\*\*Mycobacterium\*\*\* tuberculosis complex or a fragment thereof.

31. The method according to claim 30, wherein \*\*\*hybridization\*\*\* of the probe defined by any one of claims 1, 2, 9 to 11, 12, 13 and 20 to 26 to amplified IS 6110 gene from a \*\*\*Mycobacterium\*\*\* tuberculosis complex and/or a fragment thereof is conducted.

32. The method according to claim 31, wherein IS 6110 gene from a \*\*\*Mycobacterium\*\*\* tuberculosis complex and/or a fragment thereof is amplified using a primer having the nucleotide sequence of SEQ ID NO:36 or. . .

34. The method according to claim 33, wherein \*\*\*hybridization\*\*\* of the probe defined by any one of claims 3, 4, 9 to 11, 14, 15 and 20 to 26. . .

37. The method according to claim 36, wherein \*\*\*hybridization\*\*\* of the probe defined by any one of claims 5, 6, 9 to 11, 16, 17 and 20 to 26. . .

40. The method according to claim 39, wherein \*\*\*hybridization\*\*\* of

the probe defined by any one of claims 7, 8, 9 to 11, 18, 19 and 20 to 26. . . .

42. A method for detecting a pathogenic microorganism, the method comprising detecting a nucleic acid from a \*\*\*Mycobacterium\*\*\* tuberculosis complex, a gonococcus, a chlamydia or HCV using the method defined by any one of claims 27 to 41.

54. A primer for amplifying IS 6110 gene from a \*\*\*Mycobacterium\*\*\* tuberculosis complex and/or a fragment thereof, which has the nucleotide sequence of SEQ ID NO:36 or 37 or a sequence. . . .

. . . NOS:13 to 16, 23 to 26 and 28 to 31; (v) a primer for amplifying IS 6110 gene from a \*\*\*Mycobacterium\*\*\* tuberculosis complex and/or a fragment thereof, which has the nucleotide sequence of SEQ ID NO:36 or 37 or a sequence. . . .

70. The kit according to claim 68 or 69, wherein the pathogenic microorganism is a \*\*\*Mycobacterium\*\*\* tuberculosis complex, a gonococcus, a chlamydia or HCV.

. . . according to claim 75, wherein the support is selected from the group consisting of a microtiter plate, a bead, a \*\*\*magnetic\*\*\* \*\*\*bead\*\*\*, a membrane and glass.

77. A method for detecting a \*\*\*Mycobacterium\*\*\* tuberculosis complex, the method comprising treating a test sample containing a \*\*\*Mycobacterium\*\*\* tuberculosis complex with muramidase to extract a nucleic acid.

L10 ANSWER 2 OF 3 USPATFULL on STN

AN 2001:67386 USPATFULL

TI Chip-based species identification and phenotypic characterization of microorganisms

IN Gingeras, Thomas R., Encinitas, CA, United States

Mack, David, Menlo Park, CA, United States

Chee, Mark S., Palo Alto, CA, United States

Berno, Anthony J., San Jose, CA, United States

Stryer, Lubert, Stanford, CA, United States

Ghandour, Ghassan, Atherton, CA, United States

Wang, Ching, San Jose, CA, United States

PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)

PI US 6228575 B1 20010508

AI US 1997-797812 19970207 (8)

RLI Continuation-in-part of Ser. No. US 1996-629031, filed on 8 Apr 1996, now abandoned

DT Utility

FS Granted

EXNAM Primary Examiner: Horlick, Kenneth R.

LREP Townsend and Townsend and Crew LLP

CLMN Number of Claims: 97

ECL Exemplary Claim: 1

DRWN 44 Drawing Figure(s); 34 Drawing Page(s)

LN.CNT 3109

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB This invention provides oligonucleotide based arrays and methods for speciating and phenotyping organisms, for example, using oligonucleotide



sequences based on the Mycobacterium tuberculosis rpoB gene. The groups or species to which an organism belongs may be determined by comparing hybridization patterns of target nucleic acid from the organism to hybridization patterns in a database.

CLM What is claimed is:

. . . substrate, said array comprising probes complementary to reference DNA or RNA sequences from a second organism; (b) obtaining a first \*\*\*hybridization\*\*\* pattern by \*\*\*hybridizing\*\*\* a target nucleic acid sequence from the first organism to the array; and (c) comparing the first \*\*\*hybridization\*\*\* pattern of the first organism to a second \*\*\*hybridization\*\*\* pattern obtained by \*\*\*hybridizing\*\*\* a target nucleic acid sequence from the second organism to the array, wherein differences between the first and second \*\*\*hybridization\*\*\* patterns are indicative that the first organism is assigned to a particular group or species.

2. The method of claim 1, wherein the second organism is \*\*\*Mycobacterium\*\*\* tuberculosis.

4. The method of claim 3, wherein the differences in \*\*\*hybridization\*\*\* patterns are indicative of resistance to an antibiotic drug.

10. The method of claim 1, wherein the \*\*\*hybridizing\*\*\* is performed in a fluid volume of 250 .mu.l or less.

. . . presence of a nucleic acid polymorphism in a patient sample, comprising the steps of: (a) determining the difference between the \*\*\*hybridization\*\*\* intensities of a nucleic acid sequence from the patient sample and a corresponding nucleic acid sequence from a wild type sample to an array of reference nucleic acid probes; (b) deriving ratios of the difference in (a) to the \*\*\*hybridization\*\*\* intensity of the wild type sample for each base position corresponding to each reference nucleic acid probe; and (c) identifying. . .

. . . of a plurality of known nucleic acid sequences, the plurality of known nucleic acid sequences being from known organisms; inputting \*\*\*hybridization\*\*\* patterns for the plurality of known nucleic acid sequences, each \*\*\*hybridization\*\*\* pattern indicating \*\*\*hybridization\*\*\* of subsequences of the known nucleic acid

sequence

to subsequences of a reference nucleic acid sequence; inputting a \*\*\*hybridization\*\*\* pattern for a sample nucleic acid sequence from the organism indicating \*\*\*hybridization\*\*\* of subsequences of the sample nucleic acid sequence to subsequences of the reference nucleic acid sequence; comparing the \*\*\*hybridization\*\*\* pattern for the sample nucleic acid sequence to the \*\*\*hybridization\*\*\* patterns for the plurality of known nucleic acid sequences; and assigning a particular group to which the organism belongs according to the group of at least one of the known nucleic acid sequences that has a \*\*\*hybridization\*\*\* pattern that most closely matches the \*\*\*hybridization\*\*\* pattern of the sample nucleic acid sequence at specific locations.

21. The method of claim 18, further comprising the step of normalizing \*\*\*hybridization\*\*\* intensities of the \*\*\*hybridization\*\*\* patterns of the sample and known nucleic acid sequences using linear regression.

23. The method of claim 18, further comprising the step of generating a database of the \*\*\*hybridization\*\*\* patterns for the plurality of known nucleic acid sequences.

24. The method of claim 18, wherein the reference nucleic acid sequence is from \*\*\*Mycobacterium\*\*\* tuberculosis.

28. The method of claim 18, wherein the group is a species of \*\*\*Mycobacterium\*\*\* .

31. A computer program product that assigns an organism to a group, comprising: computer code that receives as input groups. . . nucleic acid sequences, the plurality of known nucleic acid sequences being from known organisms; computer code that receives as input \*\*\*hybridization\*\*\* patterns for the plurality of known nucleic acid sequences, each \*\*\*hybridization\*\*\* pattern indicating \*\*\*hybridization\*\*\* of subsequences of the known nucleic acid

sequence

to subsequences of a reference nucleic acid sequence; computer code that receives as input a \*\*\*hybridization\*\*\* pattern for a sample nucleic acid sequence from the organism indicating \*\*\*hybridization\*\*\* of subsequences of the sample nucleic acid sequence to subsequences of the reference nucleic acid sequence; computer code that compares the \*\*\*hybridization\*\*\* pattern for the sample nucleic acid sequence to the \*\*\*hybridization\*\*\* patterns for the plurality of known nucleic acid sequences; computer code that assigns a particular group to which the organism belongs according to the groups of at least one of the known nucleic acid sequences that has a \*\*\*hybridization\*\*\* pattern that most closely matches the \*\*\*hybridization\*\*\* pattern of the sample nucleic acid sequence at specific locations; and a computer readable medium that stores the computer codes.

. . . A computerized method of assigning groups to which organisms belong utilizing a generic probe array, comprising the steps of: inputting \*\*\*hybridization\*\*\* intensities for a plurality of isolates, the \*\*\*hybridization\*\*\* intensities indicating \*\*\*hybridization\*\*\* affinity between the isolate and the generic probe array; selecting \*\*\*hybridization\*\*\* intensities that have the most variance across

the

plurality of isolates; and assigning each of the plurality of isolates to a group according to the selected \*\*\*hybridization\*\*\* intensities.

. . . 32, wherein the assigning step comprises the step of clustering the plurality of isolates into groups according to the selected \*\*\*hybridization\*\*\* intensities.

36. The method of claim 32, further comprising the step of standardizing the \*\*\*hybridization\*\*\* intensities among the plurality of isolates.

37. The method of claim 36, wherein the standardizing step comprises the step of adjusting the \*\*\*hybridization\*\*\* intensities of each isolate so that there is a common mean and variance across the plurality of isolates.

. . . product that assigns groups to which organisms belong utilizing a

generic probe array, comprising: computer code that receives as input  
\*\*\*hybridization\*\*\* intensities for a plurality of isolates, the  
\*\*\*hybridization\*\*\* intensities indicating \*\*\*hybridization\*\*\*  
affinity between the isolate and the generic probe array; computer code  
that selects \*\*\*hybridization\*\*\* intensities that have the most  
variance across the plurality of isolates; computer code that assigns a  
group to each of the plurality of isolates according to the selected  
\*\*\*hybridization\*\*\* intensities; and a computer readable medium that  
stores the computer codes.

42. A method of assigning a probability that at least a subset of a  
sample \*\*\*hybridization\*\*\* pattern is associated with one or more  
species, comprising: providing a first array of polynucleotides at known  
locations on a substrate; \*\*\*hybridizing\*\*\* a first nucleic acid to  
said first array to obtain a first \*\*\*hybridization\*\*\* pattern;  
providing a second array of polynucleotides at known locations on a  
substrate, wherein at least a subset of said polynucleotides of said  
second array comprises a subset of said polynucleotides of said first  
array; \*\*\*hybridizing\*\*\* a second nucleic acid to said second array  
to obtain a second \*\*\*hybridization\*\*\* pattern; comparing at least a  
portion of said first and second \*\*\*hybridization\*\*\* patterns and  
assigning a probability, based on said comparing, that the appearance of  
said portion in a sample \*\*\*hybridization\*\*\* pattern is associated  
with one or more species.

. . . of claim 42, further comprising repeating at least once said steps  
before said comparing step to obtain a plurality of  
\*\*\*hybridization\*\*\* patterns for use in said comparing step.

44. The method of claim 42, wherein a further \*\*\*hybridization\*\*\*  
pattern is obtained as a result of said comparing step.

45. The method of claim 44, wherein said further \*\*\*hybridization\*\*\*  
pattern is based upon similarities between said \*\*\*hybridization\*\*\*  
patterns compared in said comparing steps.

46. The method of claim 44, wherein said further \*\*\*hybridization\*\*\*  
pattern is based upon differences between said \*\*\*hybridization\*\*\*  
patterns compared in said comparing step.

47. The method of claim 44, wherein said further \*\*\*hybridization\*\*\*  
pattern is based upon similarities and differences between said  
\*\*\*hybridization\*\*\* patterns compared in said comparing step.

48. A \*\*\*hybridization\*\*\* pattern obtained by the method of claim  
42.

49. The method of claim 42, wherein said assignment of said probability  
is based upon similarities between said \*\*\*hybridization\*\*\* patterns  
compared to said comparing step.

50. The method of claim 42, wherein said assignment of said probability  
is based upon differences between said \*\*\*hybridization\*\*\* patterns  
compared to said comparing step.

. . . 51. The method of claim 42, wherein said assignment of said  
probability is based upon similarities and differences between said

\*\*\*hybridization\*\*\* patterns compared to said comparing step.

. . . of claim 43, further comprising after said comparing step calling at least one base of at least one nucleic acid \*\*\*hybridized\*\*\* to said array in at least one of said repeated steps.

54. The method of claim 42, wherein said at least one of said \*\*\*hybridization\*\*\* patterns is a bar code.

55. The method of claim 42, wherein at least one of said \*\*\*hybridization\*\*\* patterns is intensity versus nucleotide position.

56. The method of claim 42, wherein at least one of said species is a species of \*\*\*Mycobacterium\*\*\*.

57. The method of claim 56, wherein said species of \*\*\*Mycobacterium\*\*\* is *M. tuberculosis*.

. . . the presence of a nucleic acid polymorphism in a patient sample, comprising: computer code that determines the difference between the \*\*\*hybridization\*\*\* intensities of a nucleic acid sequence from the patient sample and a corresponding nucleic acid sequence from a wild type sample to an array of reference nucleic acid probes; computer code that derives ratios of the difference to the \*\*\*hybridization\*\*\* intensity of the wild type sample for each base position corresponding to each reference nucleic acid probe; computer code that . . .

. . . substrate, said array comprising probes complementary to reference DNA or RNA sequences from a second organism; (b) obtaining a first \*\*\*hybridization\*\*\* pattern by \*\*\*hybridizing\*\*\* a target nucleic acid sequence from the first organism to the array; (c) comparing the first \*\*\*hybridization\*\*\* pattern of the first organism to a second \*\*\*hybridization\*\*\* pattern obtained by \*\*\*hybridizing\*\*\* a target nucleic acid sequence from the second organism to the array; (d) deriving one or more sets of differences between the first and second \*\*\*hybridization\*\*\* patterns; (e) comparing the set of differences to a data base comprising sets of differences correlated with speciation of organisms. . .

62. The method of claim 61, wherein the second organism is \*\*\*Mycobacterium tuberculosis\*\*\*.

70. The method of claim 61, wherein the \*\*\*hybridizing\*\*\* is performed in a fluid volume of 250 uL or less.

. . . nucleic acid sequence from the second organism is labeled, and the label is selected from the group consisting of biotin, \*\*\*magnetic\*\*\* \*\*\*beads\*\*\*, fluorescent dyes, radiolabels, enzymes, colorimetric labels and plastic beads.

. . . nucleic acid sequence from the second organism is labeled, and the label is selected from the group consisting of biotin, \*\*\*magnetic\*\*\* \*\*\*beads\*\*\*, fluorescent dyes, radiolabels, enzymes, colorimetric labels and plastic beads.

. . . disease is caused by a bacteria selected from the group consisting of *Escherichia coli*, *Salmonella*, *Shigella*, *Klebsiella*, *Pseudomonas*, *Listeria monocytogenes*, \*\*\*Mycobacterium tuberculosis\*\*\*,

\*\*\*Mycobacterium\*\*\* avium-intracellulare, Yersinia, Francisella, Pasteurella, Brucella, Clostridia, Bordetella pertussis, Bacteroides, Staphylococcus aureus, Streptococcus pneumonia, B-Hemolytic strep., Corynebacteria, Legionella, Mycoplasma, Ureaplasma, Chlamydia, . . .  
disease is caused by a bacteria selected from the group consisting of Escherichia coli, Salmonella, Shigella, Klebsiella, Pseudomonas, Listeria monocytogenes, \*\*\*Mycobacterium\*\*\* tuberculosis,

\*\*\*Mycobacterium\*\*\* avium-intracellulare, Yersinia, Francisella, Pasteurella, Brucella, Clostridia, Bordetella pertussis, Bacteroides, Staphylococcus aureus, Streptococcus pneumonia, B-Hemolytic strep., Corynebacteria, Legionella, Mycoplasma, Ureaplasma, Chlamydia, . . .

substrate, said array comprising probes complementary to reference DNA or RNA sequences from a second organism; (b) obtaining a first

\*\*\*hybridization\*\*\* pattern by \*\*\*hybridizing\*\*\* a target nucleic acid sequence from the first organism to the array; and (c) comparing the first \*\*\*hybridization\*\*\* pattern of the first organism to a second \*\*\*hybridization\*\*\* pattern obtained by \*\*\*hybridizing\*\*\* a target nucleic acid sequence from the second organism to the array, wherein differences between the first and second \*\*\*hybridization\*\*\* patterns are indicative of phenotypic information assigned to the first organism.

87. The method of claim 2, wherein the reference DNA or RNA sequences are selected from the \*\*\*Mycobacterium\*\*\* tuberculosis genome.

88. The method of claim 1 wherein the differences in \*\*\*hybridization\*\*\* patterns are indicative of resistance to an antibiotic drug.

89. A computerized method of assigning an organism to a group, comprising the steps of: inputting \*\*\*hybridization\*\*\* patterns for a plurality of organisms, each of the organisms belonging to a known group, each \*\*\*hybridization\*\*\* pattern indicating \*\*\*hybridization\*\*\* of subsequences of the organism belonging to a known group to subsequences of a reference nucleic acid sequence; inputting a \*\*\*hybridization\*\*\* pattern for a sample nucleic acid sequence from an organism not assigned to a group indicating \*\*\*hybridization\*\*\* of subsequences of the sample nucleic acid sequence to subsequences of the reference nucleic acid sequence; comparing the \*\*\*hybridization\*\*\* pattern for the sample nucleic acid sequence to the \*\*\*hybridization\*\*\* patterns for the plurality of organisms, each of the organisms belonging to known group; and assigning a particular group to which the organism belongs according to the group of at least one of the organisms that has a \*\*\*hybridization\*\*\* pattern that most closely matches the \*\*\*hybridization\*\*\* pattern of the sample nucleic acid sequence at specific locations.

92. The method of claim 89, wherein the reference nucleic acid sequence is from \*\*\*Mycobacterium\*\*\* tuberculosis.

96. The method of claim 89, wherein the group is a species of \*\*\*Mycobacterium\*\*\* .

97. A computer program product that assigns an organism to a group, comprising: computer code that receives as input . \*\*\*hybridization\*\*\* patterns for a plurality of organisms, each of the organisms belonging

to a known group, each \*\*\*hybridization\*\*\* pattern indicating  
 \*\*\*hybridization\*\*\* of subsequences of the organism belonging to a  
 known group to subsequences of a reference nucleic acid sequence;  
 computer code that receives as input a \*\*\*hybridization\*\*\* pattern  
 for a sample nucleic acid sequence from an organism not assigned to a  
 group indicating \*\*\*hybridization\*\*\* of subsequences of the sample  
 nucleic acid sequence to subsequences of the reference nucleic acid  
 sequence; computer code that compares the \*\*\*hybridization\*\*\*  
 pattern for the sample nucleic acid sequence to the  
 \*\*\*hybridization\*\*\* patterns for the plurality of organisms, each  
 organism belonging to a known group; computer code that assigns a  
 particular group to which the organism belongs according to the group of  
 at least one of the organisms that has a \*\*\*hybridization\*\*\* pattern  
 that most closely matches the \*\*\*hybridization\*\*\* pattern of the  
 sample nucleic acid sequence at specific locations; and a computer  
 readable medium that stores the computer codes.

L10 ANSWER 3 OF 3 USPATFULL on STN  
 AN 1998:111760 USPATFULL  
 TI Mycobacterial nucleic acid hybridization probes and methods of use  
 IN Guesdon, Jean-Luc, Paris, France  
 Thierry, Dominique, Boulogne, France  
 Ullman, Agnes, Paris, France  
 Gicquel, Brigitte, Paris, France  
 Brisson-Noel, Anne, Paris, France  
 PA Institut Pasteur, Paris, France (non-U.S. corporation)  
 PI US 5807672 19980915  
 AI US 1995-487651 19950607 (8)  
 RLI Continuation of Ser. No. US 1992-829016, filed on 14 Apr 1992, now  
 patented, Pat. No. US 5597911  
 PRAI FR 1989-11665 19890906  
 FR 1990-2676 19900302  
 DT Utility  
 FS Granted  
 EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Tung, Joyce  
 LREP Oblon, Spivak, McClelland, Maier & Neustadt, P.C.  
 CLMN Number of Claims: 21  
 ECL Exemplary Claim: 1  
 DRWN 9 Drawing Figure(s); 10 Drawing Page(s)  
 LN.CNT 1173  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
 AB Fragments of nucleic acids derived from an appropriate mycobacteria  
 genome, particularly Mycobacterium tuberculosis, their applications in  
 the diagnosis of mycobacteria infections, as well as plasmides  
 containing said fragments. The nucleotidic sequence is comprised of a  
 nucleotidic sequence repeated in the genome of a mycobacterium and  
 specific of the bacillus of tuberculosis and is characterized by a  
 strong hybridation with M. tuberculosis.  
 CLM What is claimed is:  
 . . . provided that said nucleotide sequence in which nucleotides have been  
 deleted and said nucleotide sequence which contains additional  
 nucleotides specifically \*\*\*hybridize\*\*\* to the DNA of SEQ ID NO:3.  
 6. The DNA of claim 4, wherein said solid support comprises  
 \*\*\*magnetic\*\*\* \*\*\*beads\*\*\* .

7. A purified DNA, consisting of a nucleotide sequence of from 20 nucleotides to 1358 nucleotides in length, which \*\*\*hybridizes\*\*\* exclusively to the polynucleotide of SEQ ID NO:3 under the following conditions: prehybridizing the polynucleotide of SEQ ID NO:3 for 15 minutes at 65.degree. C.; \*\*\*hybridizing\*\*\* the purified DNA with the polynucleotide of SEQ ID NO:3 for 2 hours at 65.degree. C.; washing twice for 10. . .

. . . in SEQ ID NO:3, comprising (1) producing a recombinant cosmid library containing DNA inserts larger than 30 kb from a \*\*\*mycobacterium\*\*\* of said tuberculosis bacillus group; and (2) detecting a cosmid clone containing said repetitive sequence by \*\*\*hybridizing\*\*\* said cosmid clone to a labeled DNA of claim 1.

9. A method of detecting a tuberculosis bacillus group \*\*\*mycobacterium\*\*\* of \*\*\*Mycobacterium\*\*\* bovis BCG in a biological sample, comprising (1) contacting said biological sample with the DNA of claim 1 to obtain a \*\*\*hybridization\*\*\* product between said biological sample and said DNA; and (2) detecting said \*\*\*hybridization\*\*\* product.

12. A method of detecting a tuberculosis bacillus group \*\*\*mycobacterium\*\*\* or \*\*\*Mycobacterium\*\*\* bovis BCG in a biological sample containing DNA, comprising (1) specifically \*\*\*hybridizing\*\*\* the DNA of claim 1 with said DNA in said biological sample, to obtain a \*\*\*hybridized\*\*\* product; (2) elongating said \*\*\*hybridized\*\*\* product to produce an elongation product having two strands; (3) separating said strands; (4) repeating steps (1), (2) and (3). . .

14. A kit ready for use for detecting a tuberculosis bacillus group \*\*\*mycobacterium\*\*\* or \*\*\*Mycobacterium\*\*\* bovis BCG in a biological sample, comprising: (a) the DNA of claim 1; (b) reagents for extracting said DNA in. . . said biological sample from said biological sample; (c) reagents for amplifying DNA; (d) at least one nucleotide probe which specifically \*\*\*hybridizes\*\*\* to the DNA of formula SEQ ID NO:3; (e) an internal standard, comprising DNA containing a gene for resistance to. . . provided that said nucleotide sequence in which nucleotides have been deleted and said nucleotide sequence which contains additional nucleotides specifically \*\*\*hybridize\*\*\* to the DNA of formula SEQ ID NO:3; and (f) a probe which specifically \*\*\*hybridizes\*\*\* to said DNA of said internal standard.

16. The kit of claim 14, further comprising means for making \*\*\*hybridization\*\*\* visible.

19. A method of detecting a tuberculosis bacillus group \*\*\*mycobacterium\*\*\* or \*\*\*Mycobacterium\*\*\* bovis BCG in a biological sample, comprising (1) contacting said biological sample with DNA selected from the group consisting of: . . . SEQ ID NO:5 and SEQ ID NO:10; and (f) SEQ ID NO:4 and SEQ ID NO:6, to obtain a \*\*\*hybridization\*\*\* product between said biological sample and said DNA providing a DNA fragment to be amplified; (2) amplifying said DNA fragment;. . .

21. Purified DNA primers for the amplification of \*\*\*mycobacterial\*\*\* DNA, selected from the group consisting of: (a) SEQ ID NO:5 and SEQ ID NO:10; and (b) SEQ ID NO:4. . .